Tackling Formalin-Fixed, Paraffin-Embedded Tumor Tissue with Next-Generation Sequencing

C.L. Corless and P.T. Spellman
Commentary on Wagle et al., p. 82

REVIEW
Exemestane for Breast Cancer Prevention: A Critical Shift?

A. DeCensi, B.K. Dunn, M. Puntoni, A. Gennari, and L.G. Ford

RESEARCH BRIEFS

ATM Mutations in Patients with Hereditary Pancreatic Cancer


Précis: Next-generation sequencing identifies inherited ATM mutations in kindreds with hereditary pancreatic ductal adenocarcinoma.

Molecular Ontogeny of Donor-Derived Follicular Lymphomas Occurring after Hematopoietic Cell Transplantation


Précis: Analysis of a donor–recipient pair with follicular lymphoma reveals the time-course of somatic mutations acquired during lymphomagenesis.
RESEARCH ARTICLES

Genomic Complexity and AKT Dependence in Serous Ovarian Cancer ............... 56

Précis: Individualized analyses of the PI3K/AKT and RAS pathways will identify ovarian cancers that may respond to AKT inhibition.

Wagle et al.

Loss of the 14-3-3σ Tumor Suppressor Is a Critical Event in ErbB2-Mediated Tumor Progression ............... 68
C. Ling, V-M-T. Su, D. Zuo, and W.J. Muller

Précis: 14-3-3σ inactivation accelerates formation and promotes metastasis of ErbB2/HER2-induced tumors.

High-Throughput Detection of Actionable Genomic Alterations in Clinical Tumor Samples by Targeted, Massively Parallel Sequencing ...................... 82

Précis: Targeted, sequencing-based profiling of archival tumor samples identifies genetic alterations that can direct personalized therapy.

ON THE COVER

Wagle and colleagues describe a method to profile clinically relevant mutations in formalin-fixed, paraffin-embedded tumor samples involving exon capture of frequently mutated or polymorphic genes followed by massively parallel sequencing. This method identifies single-nucleotide variants, insertions, deletions, and copy number alterations overlooked by current genotyping-based methods with high specificity and sensitivity. Identification of such “actionable” genetic alterations that predict response to targeted or conventional cytotoxic therapies has the potential to facilitate individualized cancer treatment in a time- and cost-effective manner. For details, please see the article by Wagle and colleagues on page 82.